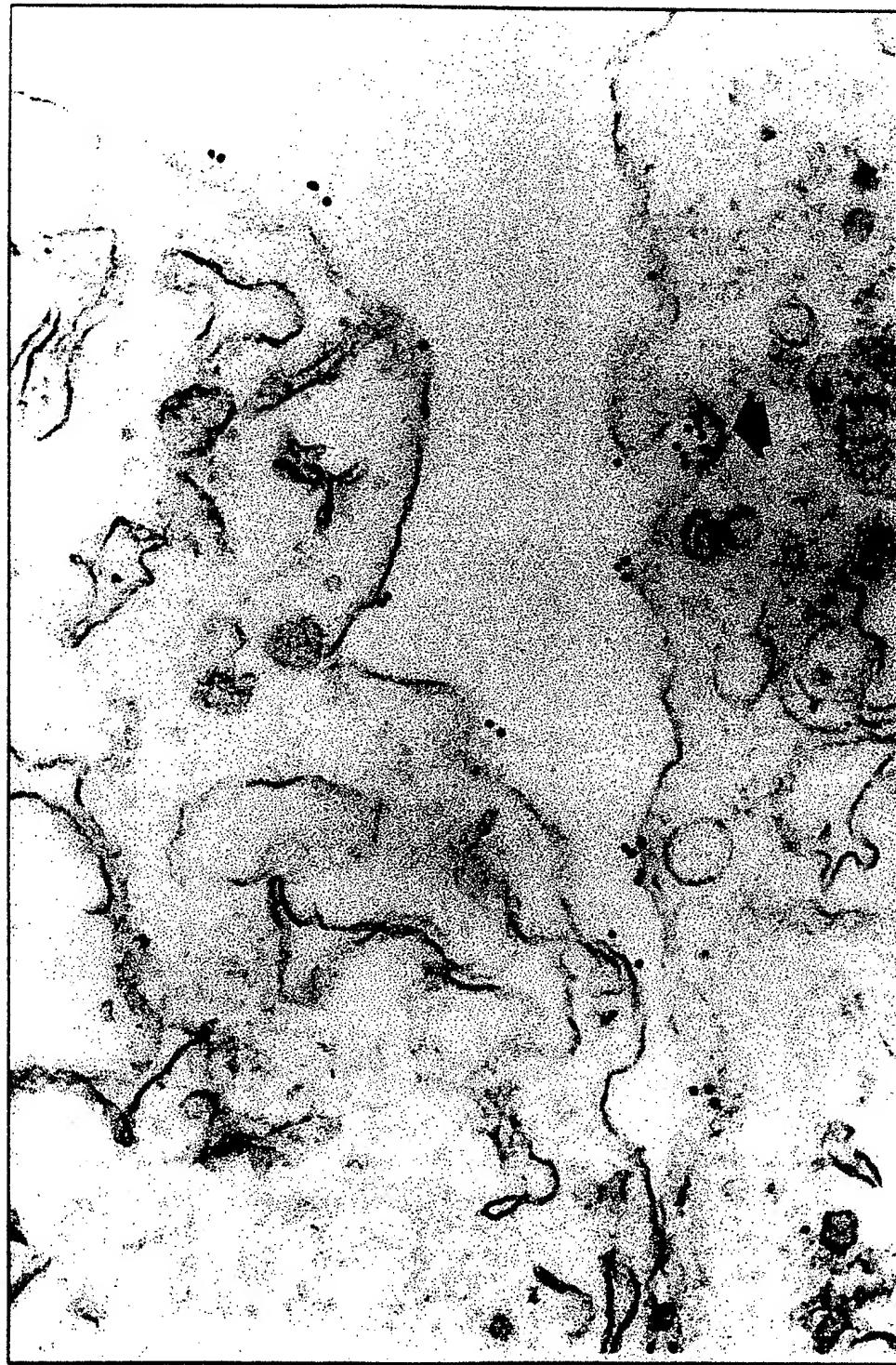


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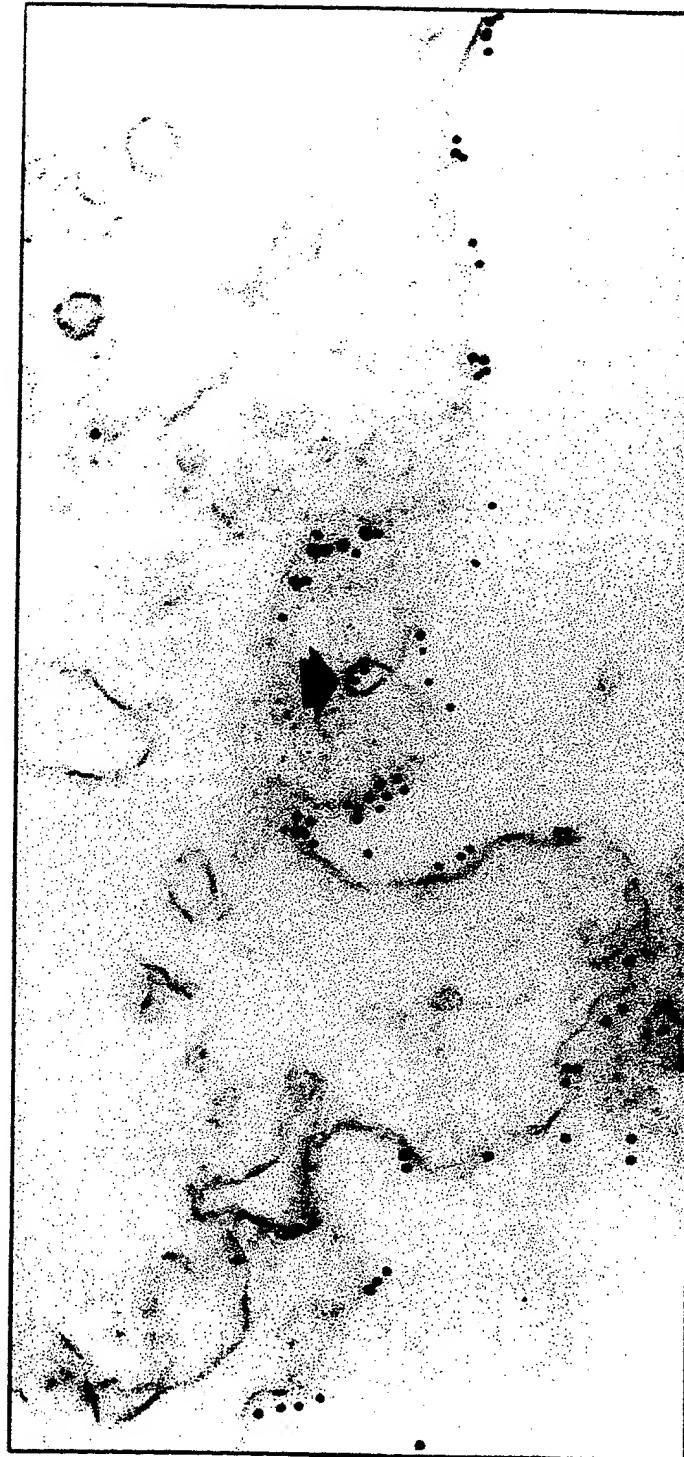
FIG. 1

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**FIG. 2**

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**FIG. 3**

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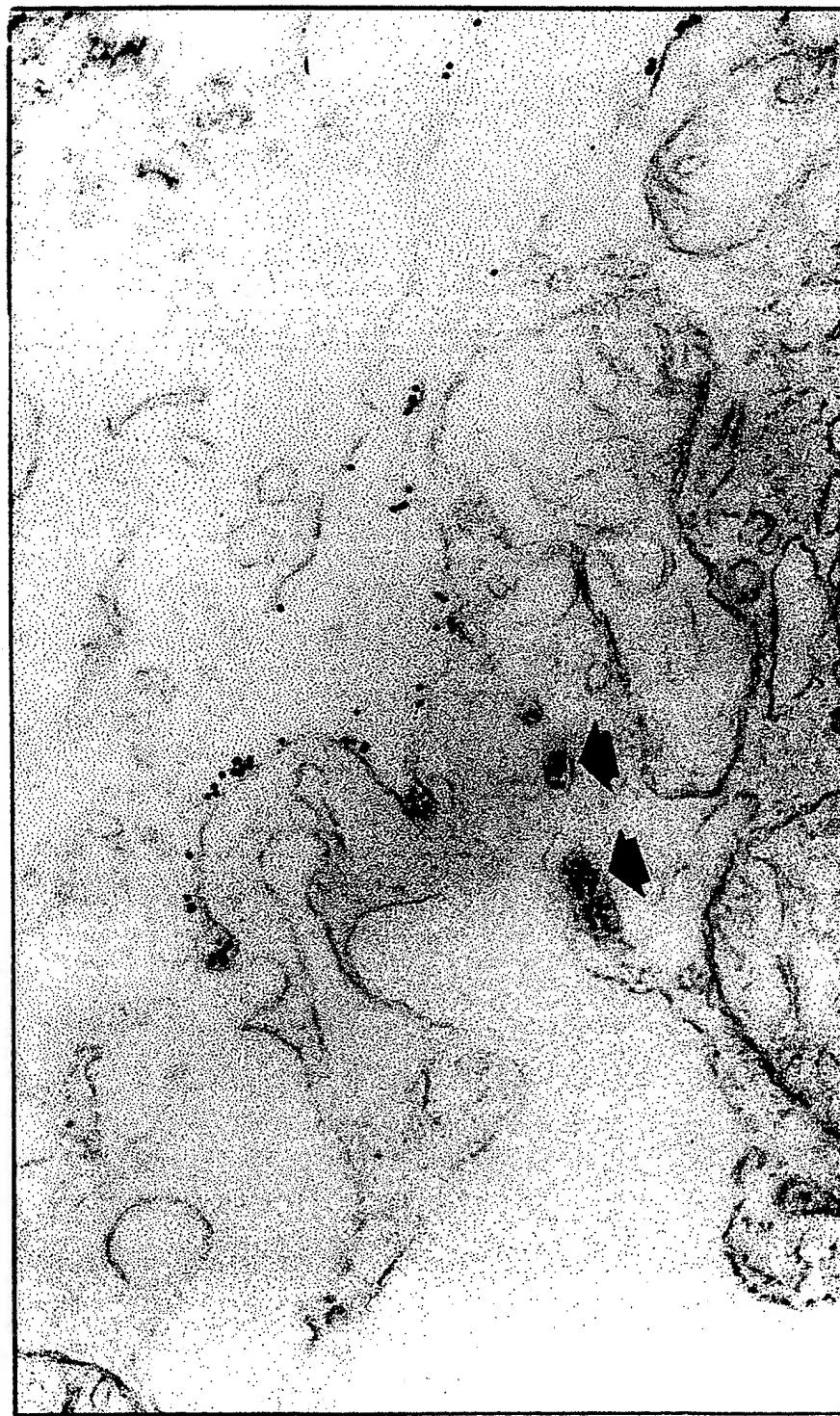


FIG. 4

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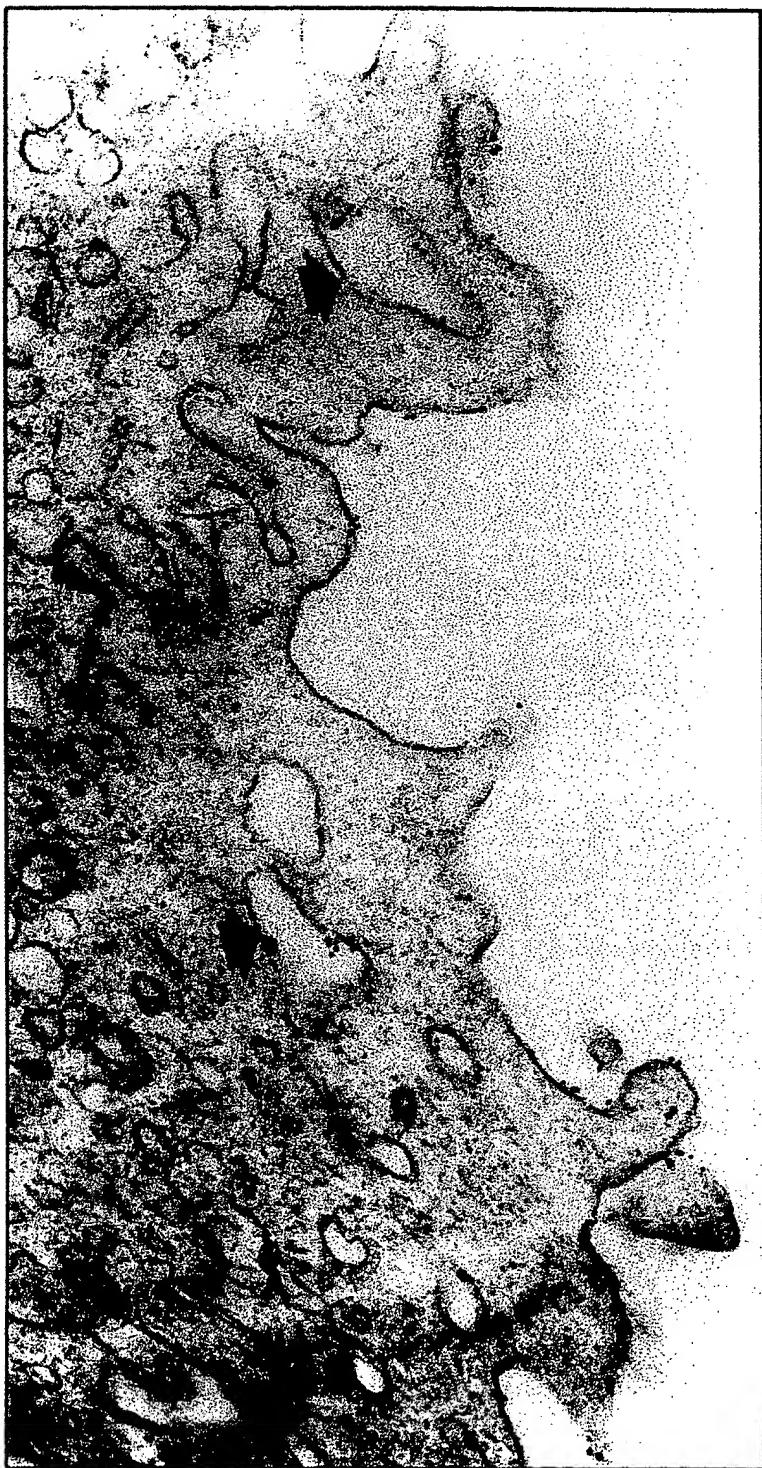


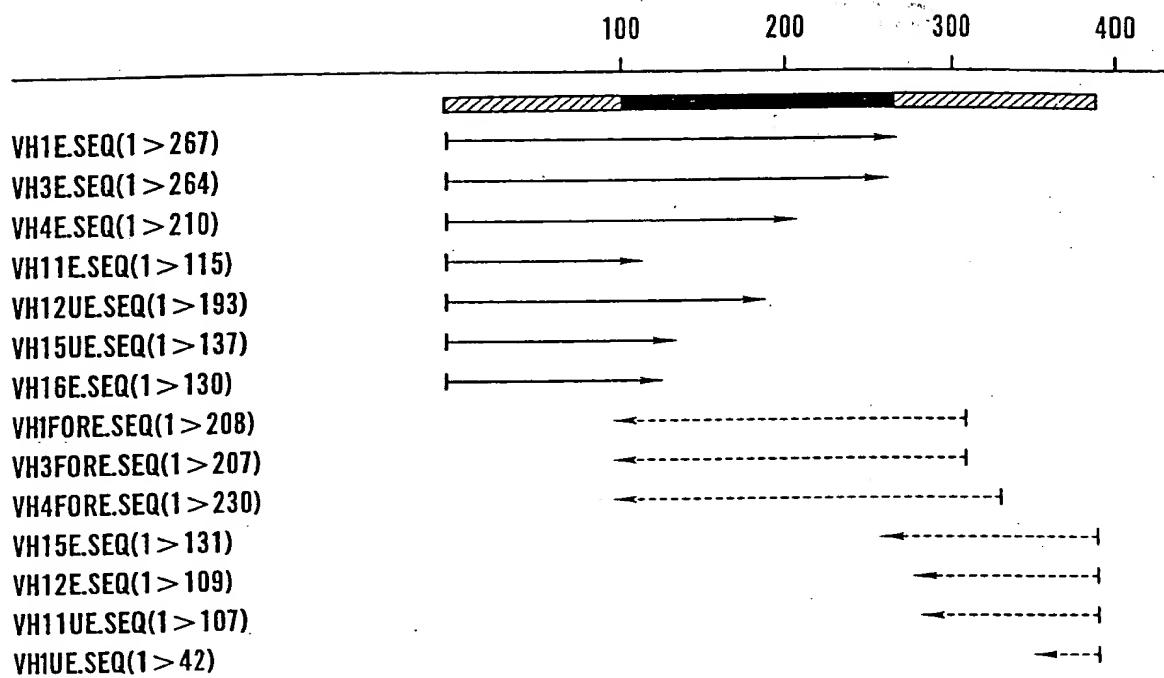
FIG. 5

TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/357,709

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**FIG. 6**

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ENZYMES: ALL 74 ENZYMES (NO FILTER)

SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

SEQ. ID. NO. 1 TCTCCCTGTCAGGAACCTGCAAGGTTCTCTCTGAGGTCCAGCTGAAACAGTCGGACCTGAACTGGTGAAG 70  
 SEQ. ID. NO. 2 AGAGGACAGTCCTGAGCTCACAGGAGAGACTCAGGTGAGGTGAGCTGAGACTGGACTTGACCACTTC  
 SEQ. ID. NO. 3 S P V R N C R C P L . G P A A T V W T . T G E  
 SEQ. ID. NO. 4 L L S G T A G V L S E V Q L Q Q S G P E L V K  
 SEQ. ID. NO. 5 L S C Q E L Q V S S L R S S C N S L D L N W . S

SEQ. ID. NO. 1 CCTGGGACTTCAGTGAGGATATCTGCAAGACCTCTGGATAACACATTCACTGAATATACCATACATGGG 140  
 SEQ. ID. NO. 2 GGACCCCTGAAAGTCACCTCCCTATAGGACGTTCTGAAGACCTATGTTAAGTGACTTATATGGTATGTGACCC  
 SEQ. ID. NO. 3 A W D F S E D I L Q D F W I H I H . I Y H T L G  
 SEQ. ID. NO. 4 P G T S V R I S C K T S G Y T F T E Y T I H W  
 SEQ. ID. NO. 5 L G L Q . G Y P A R L L D T H S L N T P Y T G

SEQ. ID. NO. 1 TGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATGGAAACATCAATCTAACAAATGGTGGTACCACTTA 210  
 SEQ. ID. NO. 2 ACTTGGCTCGGTACCTTCTCGGAACCTCACCTTGTAGTTAGGATTTGTTACCACTGGTGGAT  
 SEQ. ID. NO. 3 E A E P W K E P . V D W K H Q S . Q W W Y H L  
 SEQ. ID. NO. 4 V K Q S H G K S L E W I G N I N P N N G G T T Y  
 SEQ. ID. NO. 5 S R A M E R A L S G L E T S I L T M V V P P

SEQ. ID. NO. 1 CAATCAGAAGTTGAGGACAAGGCCACATTGACTGTAGACAAGTCCTACAGCTACAGCTACATGGAGCTC 280  
 SEQ. ID. NO. 2 GTTACGCTCTCAAGCTCCTGTTCCGGTGTAACTGACATCTGTCAGGAGTCATGTCGGATGTACCTCGAG  
 SEQ. ID. NO. 3 Q S E V R G Q G H I D C R Q V L Q Y S L H G A  
 SEQ. ID. NO. 4 N Q K F E D K A T L T V D K S S S T A Y M E L  
 SEQ. ID. NO. 5 T I R S S R T R P H . L . T S P P V Q P T W S S

SEQ. ID. NO. 1 CGCAGCCTAACATCTGAGGATTCAGCTCTATTTGAGCTGGTGGAACTTGAATACCTGGGGCC 350  
 SEQ. ID. NO. 2 GCGTCCGATTGTAGACTCTAACAGCTCAGATAATAACACGTCGACCAACCTTGAAACTGATGACCCCGG  
 SEQ. ID. NO. 3 P Q P N I . G F C S L L L C S W L E L . L L G P  
 SEQ. ID. NO. 4 R S L T S E D S A V Y Y C A A G W N F D Y W G  
 SEQ. ID. NO. 5 A A . H L R I L Q S I I V Q L V G T L T T G A

SEQ. ID. NO. 1 AAGGCACCAACTCTCACAGTCCTCTAGCCAAAAAGACACCC 391  
 SEQ. ID. NO. 2 TTCCGTTGGTGGAGAGTGTCAAGAGGAGTGGTTTGCTGTGGG  
 SEQ. ID. NO. 3 R H H S H S L L S Q N D T  
 SEQ. ID. NO. 4 Q G T T L T V S S A K T T P  
 SEQ. ID. NO. 5 K A P L S Q S P Q P K R H P

FIG. 7

FIG. 7

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**LIPMAN-PEARSON PROTEIN ALIGNMENT**  
**KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12**

SEQ1(1>115) J591VH.PRO	SEQ2(1>125) MUVHIIA.PRO	SIMILARITY INDEX	GAP NUMBER	GAP LENGTH	CONSENSUS LENGTH
(1>115)	(1>125)	75.6	2	10	125

EVQLQSGPELVKPGTSVRISCKTSGYTFTEYTI-HWVKQSHGKSLEWIGNINPNNGIT  
 EVQLQSGPELVKPG:SV:ISCK:SGYTF:Y: :WVKQS.GKSLEWIG:INP.NGGT:  
 EVQLQSGPELVKPGASVKISCKASGYTFDYYMNNWVKOSPGKSLEWIGDINPGNGITS  
 YNQKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WIFDYWGQGTT  
 YNQKF.:KATLTVDKSSSTAYM:L.SLTSEDSAVYYCA G ..FDYWGQGTT  
 YNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARGYSSYMAYYAFDYWGQGTT  
 LTVSS  
 :TVSS  
 VIVSS

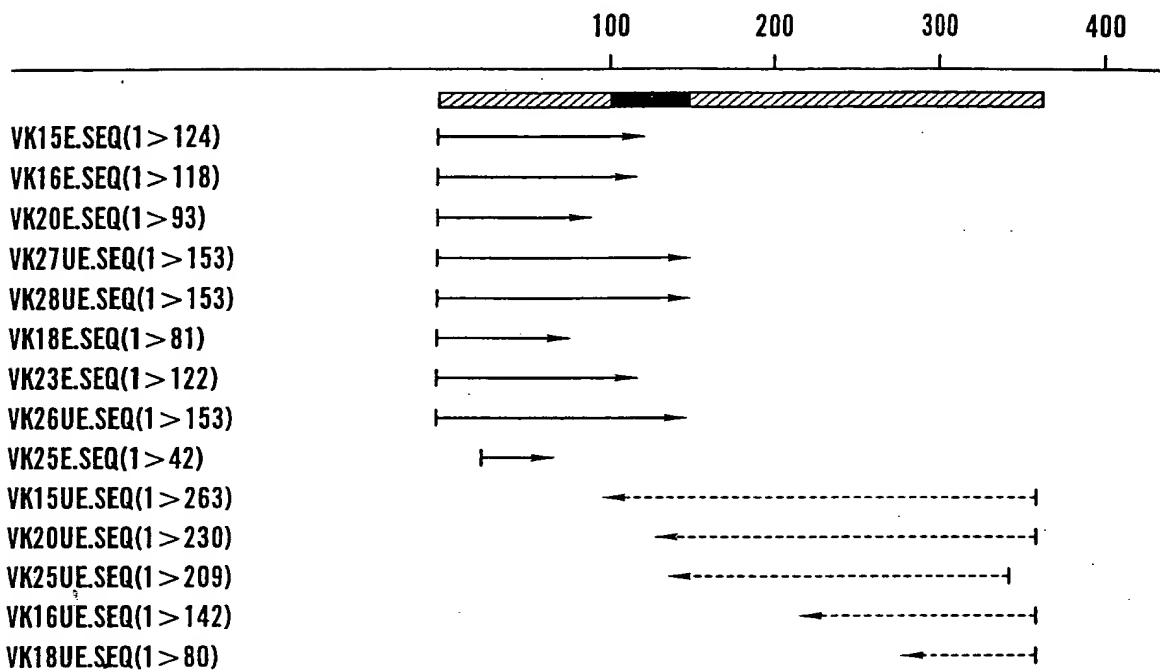
*FIG. 8*

TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/357,709

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**FIG. 9**

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ENZYMES: ALL 74 ENZYMES (NO FILTER):  
SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

Alu | Hph I

SEQ. ID. NO. 9 TTATATGGAGCTGATGGAACATTGTAATGACCAATCTCCAAATCCATGTCAGTCAGTAGGAGAGA 70

SEQ. ID. NO. 10 AATATACTCGACTACCCCTGTAACATTACTGGGTTAGAGGGTTAGGTACAGGTACAGTCATCCCTCT

SEQ. ID. NO. 11 L Y G A D G N I V M T Q S P K S M S M S V G E

SEQ. ID. NO. 12 Y M E L M G T L . . P N L P N P C P C Q . E R

SEQ. ID. NO. 13 I I W S . W E H C N D P I S Q I H V H V S R R E

Hae III  
Bsr I

SEQ. ID. NO. 9 GGGTCACCTTGACCTGCAAGGCCAGTGAGAAATGCGGTTACTTATGTTCTGGATCAACAGAAACCGAGA 140

SEQ. ID. NO. 10 CCCAGTGGAACTGGACGGTCCGGTCACTCTAACCCAATGAATAACAAAGGACCATAGTGTCTGGCT

SEQ. ID. NO. 11 R V T L T C K A S E N V V T Y V S W Y Q Q K P E

SEQ. ID. NO. 12 G S P . P A R P V R M W L L M F P G I N R N Q

SEQ. ID. NO. 13 G H L D L Q G Q . E C G Y L C F L V S T E T R

Ava II Mbo I

Hpa II Bsr I Dpn I

Rsa I Sau96 I Bsa0 I

Pvu I

Alw26 I Fok I

SEQ. ID. NO. 9 GCAGTCCTAAACCTGATATAGGGCATCCAACCGGTACACTGGGTOCCCGATGCTCACAGG 210

SEQ. ID. NO. 10 CGTCAGAGGATTGACCACTATGCCCCGTTAGGTGGCCATGTGACCCCCAGGGCTAGCGAAGTGTCCG

SEQ. ID. NO. 11 Q S P K L L I Y G A S N R Y T G V P D R F T G

SEQ. ID. NO. 12 S S L L N C . Y T G H P T G T L G S P I A S Q A

SEQ. ID. NO. 13 A V S . T A D I R G I Q P V H W G P R S L H R

Mbo I Dpn I Bsp6 II Mbo II Eco57 I

SEQ. ID. NO. 9 ATGGGATCTGCAACAGAATTCACTCTGACCATCAGCAGTGTGCAAGGCTTGCAGATTATCACT 280

SEQ. ID. NO. 10 TCACCTAGACGTTGCTAAAGTGAGACTGGTATGCTCACAOGTGGACTTCTGGAACGCTAAATAGTGA

SEQ. ID. NO. 11 S G S A T D F T L T I S S V Q A E D L A D Y H

SEQ. ID. NO. 12 V D L Q Q I S L . P S A V C R L K T L Q I I T

SEQ. ID. NO. 13 Q W I C N R F H S D H Q Q C A G . R P C R L S L

Ava II

Alu I Rsa I Sau96 I Alu I

SEQ. ID. NO. 9 GTGGACAGGGTTACACCTATCCGACACGGTCCGAGGGGGGACCAAGCTGGAAATAAAACGGCTGATGC 350

SEQ. ID. NO. 10 CACCTGTCCTAAATGTCGATAGGCTGTCAGGCTCCTGGTTCGACCTTATTTGCCCCGACTAG

SEQ. ID. NO. 11 C G Q G Y S Y P Y T F G G G T K L E I K R A D A

SEQ. ID. NO. 12 V D R V T A I R T R S E G G P S W K . N G L M

SEQ. ID. NO. 13 W T G L Q L S V H V R R G D Q A G N K T G . C

FIG. 10

## TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/357,709

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**LIPMAN-PEARSON PROTEIN ALIGNMENT**  
**KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12**

SEQ1(1>107) J591VK.PRO (1>107)	SEQ2(1 > 1 1 1) MUVKV.PRO (1>109)	SIMILARITY INDEX 60.4	GAP NUMBER 2	GAP LENGTH 2	CONSENSUS LENGTH 109
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NTIVMTQSPKSMMSMSVGERVILTCKAS-ENVVITYVSWYQQKPEQSPKLLIYGASNRYTGVP  
 :I MTQSP.S:S S:G:RVT:TC:AS ::: .Y: :WYQQKP. SPKLLIY AS. .:GVP  
 DIQMTQSPSSLSASLGDRVTITCRASQDDISNYLNWYQQKPGGSPKLLIYYASRLHSGVP  
 DRFTGSGSATDFTLTISVQAEDLADYHOGQGYSY-PYTFGGGTKEIK  
 .RF:GSGS:TD: :LTIS:::ED:A.Y C QG : P TFGGGTKEIK  
 SRFSGSGSGIDYSLTISNLEQEDIATYFOQQGNTLPPRTFGGGTKEIK

↘ 10            ↘ 20            ↘ 30            ↘ 40            ↘ 50  
 ↗ 10            ↗ 20            ↗ 30            ↗ 40            ↗ 50            ↗ 60  
 ↘ 60            ↘ 70            ↘ 80            ↘ 90            ↘ 100  
 ↗ 70            ↗ 80            ↗ 90            ↗ 100

**FIG. 11**